IN THE SPECIFICATION

Please amend the paragraph beginning at page 15, line 6 as follows:

--For instance, the SPLASH algorithm may be used. Full details of the SPLASH algorithm are given in Califano, A., "SPLASH: Structural Pattern Localization Algorithm by Sequential Histograming," Bioinformatics 16, 341-357, 2000, the disclosure of which is incorporated by reference herein. ~~Preprints are available at http://www.research.ibm.com/topics/popups/deep/math/html/splashexternal.PDF.~~ In that paper, SPLASH was introduced as an algorithm to discover patterns in strings, where all possible relative strings alignment are allowed. Also, a density constraint is introduced to limit the impact of random matches occurring over large distances on the string. For the equivalent association discovery problem, relevant in this context, the approach is analogous, as each row in the matrix is equivalent to a string. However, the strings are prealigned in the present case, meaning that the strings are aligned with the genes to which they correspond. In addition, the density constraint criteria introduced in the SPLASH paper is no longer meaningful here, as the first and last genes are as likely to form patterns as two corresponding to contiguous matrix columns.--

Please amend the paragraph beginning at page 26, line 4 as follows:

--Three methods are studied: The pattern discovery method (PD) of the present invention; the support vector machine (SVM) method disclosed in Brown, M.P.S. et al., "Support Vector Machine Classification of Microarray Gene Expression Data," University of California Technical Report USCC-CRL-99-09, 1999~~, which is available at: http://www.cse.ucsc.edu/research/compbio/genex~~; and the gene by gene method (GBG) disclosed in Golub, T.R. et al., "Molecular Classification of Cancer: Class Discovery and Class Prediction by Gene Expression Monitoring," Science, Vol 286, pp. 531-537, 1999. For each given phenotype, its complement in the NCI-60 was used, excluding the samples whose phenotype cannot be accurately determined (neutral samples), as the control set.--